SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Margaret K. Hostetter, et al.

(ii) TITLE OF INVENTION: HUMAN COMPLEMENT C3-DEGRADING PROTEINASE FROM *STREPTOCOCCUS PNEUMONIAE*

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:
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(D) STATE: MINNESOTA
(E) COUNTRY: USA
(F) ZIP: 55401

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) PRIORITY APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US98/08281
(B) FILING DATE: 24-APR-1998
(C) CLASSIFICATION:

(vii) PRIORITY APPLICATION DATA:
(A) APPLICATION NUMBER: 60/044,316
(B) FILING DATE: 24-APRIL-97
(C) CLASSIFICATION:

(viii) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/403,422
(B) FILING DATE: 19-OCT-1999
(C) CLASSIFICATION:

(ix) ATTORNEY/AGENT INFORMATION:
(A) NAME: MUETING, ANN M.
(B) REGISTRATION NUMBER: 33,977
(C) REFERENCE/DOCKET NUMBER: 110.00580101

(x) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 726 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAATGTAA ATCAGATTGT ACGGATTATT CCTACTTTAA AAGCTAATAA TAGAAAATTA 60
AATGAAACAT TTTATATTGA AACCCTTGGA ATGAAGGCCT TGTTAGAAGA ATCGGCCTTT 120
CTGTCACTAG GTGACCAAAC GGGTCTTGAA AAGCTGGTTT TAGAAGAAGC TCCCAGTATG 180
CGTACTCGTA AGGTAGAGGG AAGAAAAAAA CTAGCTAGAT TGATTGTCAA GGTGGAAAAT 240
CCCTTAGAAA TTGAAGGAAT CTTATCTAAA ACAGATTCGA TTCATCGATT ATATAAAGGT 300
CAAAATGGCT ACGCTTTTGA AATTTTCTCA CCAGAAGATG ATTTGATTTT GATTCATGCG 360
GAAGATGACA TAGCAAGTCT AGTAGAAGTA GGAGAAAAGC CTGAATTTCA AACAGATTTG 420
GCATCAATTT CTTTAAGTAA ATTTGAGATT TCTATGGAAT TACATCTCCC AACTGATATC 480
GAAAGTTTCT TGGAATCATC TGAAATTGGG GCATCCCTTG ATTTTATTCC AGCTCAGGGG 540
CAGGATTTGA CTGTGGACAA TACGGTTACC TGGGACTTAT CTATGCTCAA GTTCTTGGTC 600
AATGAATTAG ACATAGCAAG TCTTCGCCAG AAGTTTGAGT CTACTGAATA TTTTATTCCT 660
AAGTCTGAAA AATTCTTCCT TGGTAAAGAT AGAAATAATG TTGAATTGTG GTTTGAAGAA 720
GTATGA 726

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Val Asn Gln Ile Val Arg Ile Ile Pro Thr Leu Lys Ala Asn
1 5 10 15

Asn Arg Lys Leu Asn Glu Thr Phe Tyr Ile Glu Thr Leu Gly Met Lys
20 25 30

Ala Leu Leu Glu Glu Ser Ala Phe Leu Ser Leu Gly Asp Gln Thr Gly
35 40 45

Leu Glu Lys Leu Val Leu Glu Glu Ala Pro Ser Met Arg Thr Arg Lys
50 55 60

Val Glu Gly Arg Lys Lys Leu Ala Arg Leu Ile Val Lys Val Glu Asn
65 70 75 80

Pro Leu Glu Ile Glu Gly Ile Leu Ser Lys Thr Asp Ser Ile His Arg

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                85                  90                  95

Leu Tyr Lys Gly Gln Asn Gly Tyr Ala Phe Glu Ile Phe Ser Pro Glu
            100                 105                 110

Asp Asp Leu Ile Leu Ile His Ala Glu Asp Asp Ile Ala Ser Leu Val
        115                 120                 125

Glu Val Gly Glu Lys Pro Glu Phe Gln Thr Asp Leu Ala Ser Ile Ser
    130                 135                 140

Leu Ser Lys Phe Glu Ile Ser Met Glu Leu His Leu Pro Thr Asp Ile
145                 150                 155                 160

Glu Ser Phe Leu Glu Ser Ser Glu Ile Gly Ala Ser Leu Asp Phe Ile
                165                 170                 175

Pro Ala Gln Gly Gln Asp Leu Thr Val Asp Asn Thr Val Thr Trp Asp
            180                 185                 190

Leu Ser Met Leu Lys Phe Leu Val Asn Glu Leu Asp Ile Ala Ser Leu
        195                 200                 205

Arg Gln Lys Phe Glu Ser Thr Glu Tyr Phe Ile Pro Lys Ser Glu Lys
    210                 215                 220

Phe Phe Leu Gly Lys Asp Arg Asn Asn Val Glu Leu Trp Phe Glu Glu
225                 230                 235                 240

Val
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CAGGAAGCTT GATCTTGAAA TTTCTATGAC TCC                                    33
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGAGAAGCTT GATCCTGTCG AAATCAAAGC AGGACG 36

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAGGAAGCTT TGAAACAATT TATATTGAAA CCC 33

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGAGAAGCTT CAAGGAAGAA TTTTTCAGAC TTAGG 35

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGGAATTCC ATATGAATGT AAATCAGATT GTACGG 36

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCCGCGGAT CCTCATACTT CTTCAAACCA CAATTC 36

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTCCCAGTA TGCGTACTCG TAAGGTAGAG GGAAGAAAAA AACTAGCTAG 50